

恶性肿瘤的癌变原理研究专栏

RUNX3基因启动子甲基化与早期非小细胞肺癌的预后

唐艳^{1,2}, 吴芳¹, 胡春宏¹

1.中南大学湘雅二医院肿瘤科, 长沙 410011; 2.长沙市八医院肿瘤科, 长沙 410001

摘要:

目的: 探讨RUNX3基因启动子甲基化与非小细胞肺癌(NSCLC)预后的关系。方法: 酚/氯仿法提取80例术后接受顺铂辅助化疗NSCLC患者的肺癌组织标本DNA, 巢氏甲基化特异性PCR (nMSP) 检测RUNX3启动子甲基化状态, 并回顾性分析甲基化状态与临床病理特征、术后无病生存、总生存的关系。结果: 80例NSCLC肿瘤样本中20例检测到RUNX3基因启动子甲基化(25.0%)。RUNX3启动子基因甲基化与病理类型相关(P=0.020), 且腺癌(36%)高于鳞癌(11%)。N分期(OR: 4.898, P<0.001)、RUNX3基因启动子甲基化(OR: 20.293, P=0.011)是影响术后无病生存的独立危险因素。单因素K-M生存分析、Cox多因素分析表明RUNX3基因甲基化(RR: 2.345, 95%CI: 1.130~4.865, P=0.022)是影响总生存的独立危险因素。结论: RUNX3基因甲基化是影响术后NSCLC无病生存和总生存的独立影响因素。

关键词: RUNX3基因; DNA甲基化; 预后; 非小细胞肺癌; 表观遗传

RUNX3 promoter hypermethylation and prognosis of early surgically resected non-small cell lung cancers

TANG Yan^{1,2}, WU Fang¹, HU Chunhong¹

1.Department of Oncology, Second Xiangya Hospital, Central South University, Changsha 410011; 2. Department of Oncology, The Eighth Hospital of Changsha, Changsha 410001, China

Abstract:

Objective To determine the relation between the promoter methylation status of RUNX3 gene and clinicopathological parameters, prognosis of non-small cell lung cancer (NSCLC). Methods We collected 80 formalin-fixed paraffin-embedded lung cancer tissue samples from NSCLC patients who received postoperative adjuvant chemotherapy with cisplatin. Genomic DNA was extracted through phenol/chloroform extraction. The methylation status of RUNX3 was determined by nested methylation-specific PCR (nMSP). We investigated the pathological and prognostic characteristics of NSCLC stratified by methylation status. Results The RUNX3 promoter methylation was observed in 20 of the 80 NSCLC samples (25.0%). Methylation of RUNX3 was more frequent in adenocarcinomas (36%) than in squamous cell carcinomas (11%) (P=0.020). In multivariate Logistic regression, positive RUNX3 methylation status (P=0.011) was found to be independent disease-free survival factor as was N stage (P<0.001). Kaplan-Meier curves showed patients with RUNX3 methylation had a significantly poorer overall survival than those without methylation (P=0.003; log-rank test). In multivariate Cox proportional hazards regression analysis, RUNX3 methylation (RR: 2.345, 95% CI: 1.30-4.865, P=0.022) was a significant independent prognostic factor for the overall survival. Conclusion RUNX3 methylation is a significant independent prognostic factor for disease-free survival and overall survival.

Keywords: RUNX3 gene DNA methylation prognosis non-small cell lung cancer epigenomics

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